

TRANSPARENT METHODS

EXPERIMENTAL MODEL AND SUBJECT DETAILS

Subjects and Methods

We conducted field research in seven different states of Mexico during 2011-12. They include Guanajuato (GTO), Hidalgo (HGO), Morelos (MOR), Puebla (PUE), Querétaro (QRO), San Luis Potosí (SLP), and Veracruz (VER). We enrolled adult males between the ages of 18 and 65 years old who identified themselves as Native Mexicans and belonging to populations speaking languages belonging to one of three different linguistic families. They include the Nahuatl (Uto-Aztecán); Chichimeca (*Úza'*, plural *Éza'r*), Otomí (*Hñähñú*), and Popoloca (Otomanguean); and Tepehua and Totonaca (Totonacan), with the language family being given in parentheses. *Úza'* and *Hñähñú* are the names by which the Chichimeca and the Otomí self-identify, respectively. Thus, these names have been used in the main text in order to respect these identities.

During the field expeditions, blood and saliva samples and genealogical data were collected from 289 men following informed consent. These men belonged to six Native Mexican ethnic groups that resided in 25 different localities ([Table S1](#)). A total of 236 men were unrelated participants through three generations, including 13 *Éza'r*, 71 Nahuas (44 from HGO, 7 from MOR, and 20 from SLP), 90 *Hñähñús* (4 from GTO, 81 from HGO, and 5 from QRO), 8 Popolocas, 28 Tepehuas, and 21 Totonacas (5 from PUE and 16 from VER). Five individuals who identified themselves in the genealogical survey as a Mestizos were excluded from the analyses. As a result, a total of 231 males participated in this study ([Table S2](#)).

The University of Pennsylvania Institutional Review Board #8, the Centro de Investigación y de Estudios Avanzados del Instituto Politécnico Nacional (Cinvestav-IPN), and

the Comisión Nacional para el Desarrollo de los Pueblos Indígenas, now named Instituto Nacional de los Pueblos Indígenas, approved the data and sample collection protocol for this project.

METHOD DETAILS

Molecular Genetic Analysis

DNA isolation

DNA from peripheral blood leukocytes and collected in EDTA-Vaccutainer® tubes was isolated using Gentra PureGene Blood Kit (Qiagen) following the recommendations of the manufacturer. Saliva cells were collected in 15mL polypropylene tubes with commercial mouthwash (Scope®) from which buccal cells were pelleted by centrifugation with an Eppendorf centrifuge 5408R using a swing-bucket A-4-44 rotor (Eppendorf AG) at 2,935g for 5 min. The buccal cells pellets were incubated with Cell Lysis Solution and Proteinase K (Qiagen) at 56°C overnight followed by the DNA isolation as previously described.

Genotyping

All samples were genetically characterized using nineteen Y-STR (Y-chromosome short tandem repeats) using the AmpFlSTR Y-filer PCR amplification kit (Applied Biosystems) and two additional Y-STRs (DYS388 and DYS426) in a Custom STR-SNP assay (Applied Biosystems). In addition, six fragment length polymorphisms (M17, M60, M91, M139, M175, and M186) were amplified using a custom STR-SNP assay (Applied Biosystems). The samples were amplified using a Verity 96-Well Fast Thermal Cycler (Applied Biosystems). The resulting amplicons were run on a ABI Prism 3130XL and fragment sizes mapped with the GeneMapper

ID v.3.2 software (Applied Biosystems). Each sample was further characterized using 21 SNPs ([Table S3](#)) with custom TaqMan genotyping assays (Applied Biosystems,) which were amplified in a C1000 Touch Thermal Cycler (Bio-Rad). The Y Chromosome Consortium-2008 (YCC) and International Society of Genetic Genealogy 2019-20 recommendations were used to determine the haplogroup nomenclature ([Karafet et al., 2008](#); [International Society of Genetic Genealogy, 2020](#)). Non-Amerindian haplogroups were assigned to haplogroups using Y-STR haplotypes with a Bayesian predictor software; assignments ~ 80% were included in the analyses ([Table S5](#)) ([Athey, 2005](#)).

Comparative Data

Y-SNP and Y-STR data from Native Mexican populations were compared to data available from published reports ([Table S7](#)). A total of 158 populations (n = 1811) from Asia, North, Central, and South America were included in the database and used for further analysis. Non-Amerindian data from Native Mexican populations were similarly compared to published data from indigenous and non-native populations ([Table S6](#)). They included 2798 individuals from Mexico, Europe (Spain, France, and Italy), the Kingdom of Bahrain, Tunisia, and Morocco.

QUANTIFICATION AND STATISTICAL ANALYSIS

Data Analysis

A number of statistical methods were used to analyze the Y-STR data. They included haplotype diversity (h), pairwise differences, and analysis of molecular variance (AMOVA) which were made with Arlequin v.3.5 ([Excoffier and Lischer, 2010](#)) using 1000 permutations. Intrapopulation variances (V_p) were estimated as described in [Kayser et al., \(2001\)](#). Genetic

distances (R_{ST} values) were estimated with Arlequin v.3.5 (Excoffier and Lischer, 2010) using an exact test of population differentiation with 10,000 steps in Markov chain and 1000 demorization steps and visualized in a multidimensional scaling plot (MDS) using SPSS v.11 (IBM SPSS, 2001).

NRY Phylogeography

The phylogenetic relationships among Y-STR haplotypes were constructed using median-joining (MJ) and reduced-median options in Network v.5.0 (Bandelt et al., 1999) and visualized with Network Publisher. The network analyses were generated using 17-YSTR; DYS385a/b was excluded from all the analyses performed given that it represents a duplicate STR locus. DYS839II value was obtained using the subtraction between DYS389II and DYS389I. The Y-STR loci were weighted using the inverse of variance for each one of them.

The demographic history of the populations, coalescence times, and mutation rates were inferred using Beast2 v.2.4.3, and Batwing (Bouckaert et al., 2014; Wilson et al., 2003). The coalescent times for founding lineages were assessed using Network v.5.0 software (Bandelt et al., 1999) with p-statistics. A rate of one mutation every 453 years was used; this estimate was generated by taking the inverse per generation mutation rate of each locus multiplied by the number of loci and by generation time, or 25 years (Chandler, 2006). Each haplotype was connected to all other haplotypes from which it differed by one repeat unit step at a single microsatellite locus.

Markov Chain Monte Carlo (MCMC) methods were also used to infer the times of more recent common ancestor (TMRCA) and the Y-chromosomal lineage histories. For the inference using Batwing software (Bayesian Analysis of Trees With Internal Node Generation) (Wilson et

al., 2003) a constant population growth size model was used. Other settings for the Bayesian methods included the following: gamma distribution (1.47, 2130) for the microsatellite mutation rate (Zhivotovsky et al., 2004), gamma (1, 0.0001) for the initial effective population size, and gamma distribution (2,400) for the population growth rate alpha *per* generation as described by Contu et al. (2008). Results obtained with this software were post-processed using the Batwing library implemented by the authors in the R software (R Core Team, 2019). Despite other studies using 25 years as generation time (Thomson et al., 2000) we explored different times (i.e., 18, 20, and 25 years) in order to obtain more reliable values.

The Phylogenetic-Coalescent analysis multi-locus performed in Beast2 v.2.4.3 (Bouckaert et al., 2014) and the implementing phylogenetic analysis for microsatellites (BEASTvntr) (Wu and Drummond, 2011) allowed inference of the TMRCA based on the allelic frequencies of haplogroup-integrated microsatellites. Estimates for Q-M3 and Q-L54 haplogroups were determined in Arlequin v3.5 (Excoffier and Lischer, 2010). Mutation rates for the microsatellites used (DYS19 2.24, DYS389-I 2.93, DYS389-II 4.12, DYS390 2.11, DYS391 2.45 DYS392 5.19, DYS393 1.05, DYS437 1.22, DYS438 3.75 DYS439 5.45 DYS448 1.52, DYS456 4.29, DYS458 6.36, DYS635 6.36, YGATA-H4 3.03), relaxed clock model, and Yule tree model were the priors for these analyses.

Two reference points were used to tree calibration. The first one located in the node of haplogroup Q-M3 dated to 20,000 years BP, based on mitochondrial lineages reported by Schurr and Sherry (2004). The second, located in haplogroup Q-L54 was dated at 8720 years BP, according to the last connection with the Altai population from which this haplogroup is derived (Dulik et al., 2012b). Three independent runs of 10 million MCMCs were conducted, with a 10% burn-in, and resampling every 10,000 states. The coverage of each run was verified in Tracer

v.1.7.1 ([Rambaut and Drummond, 2007](#)) with a minimum ESS value of 200; the results of each run were combined in LogCombiner v.1.7 ([Drummond and Rambaut, 2007](#)). Finally, the maximum credibility tree was obtained with the program TreeAnnotator v.1.6.1 ([Helfrich et al., 2017](#)), and visualized in FigTree v.1.4.4 ([Rambaut, 2018](#)).

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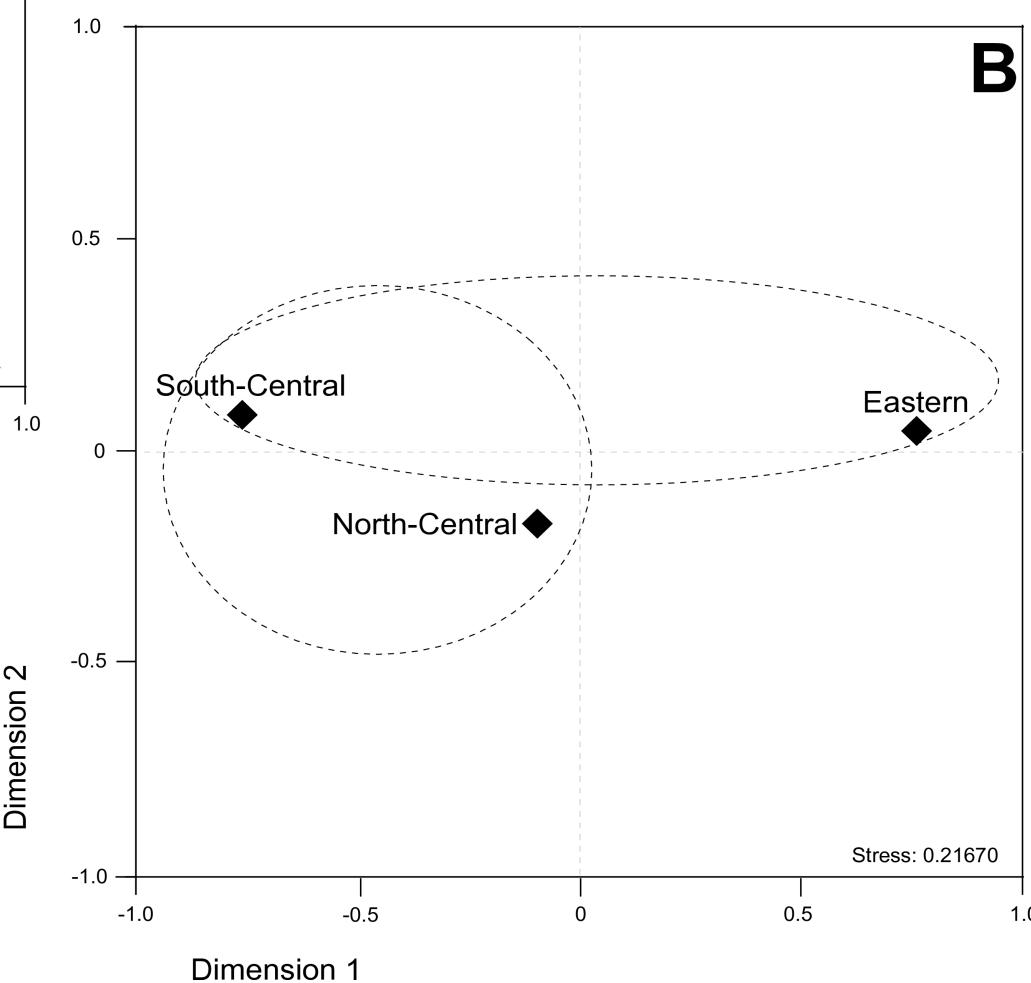
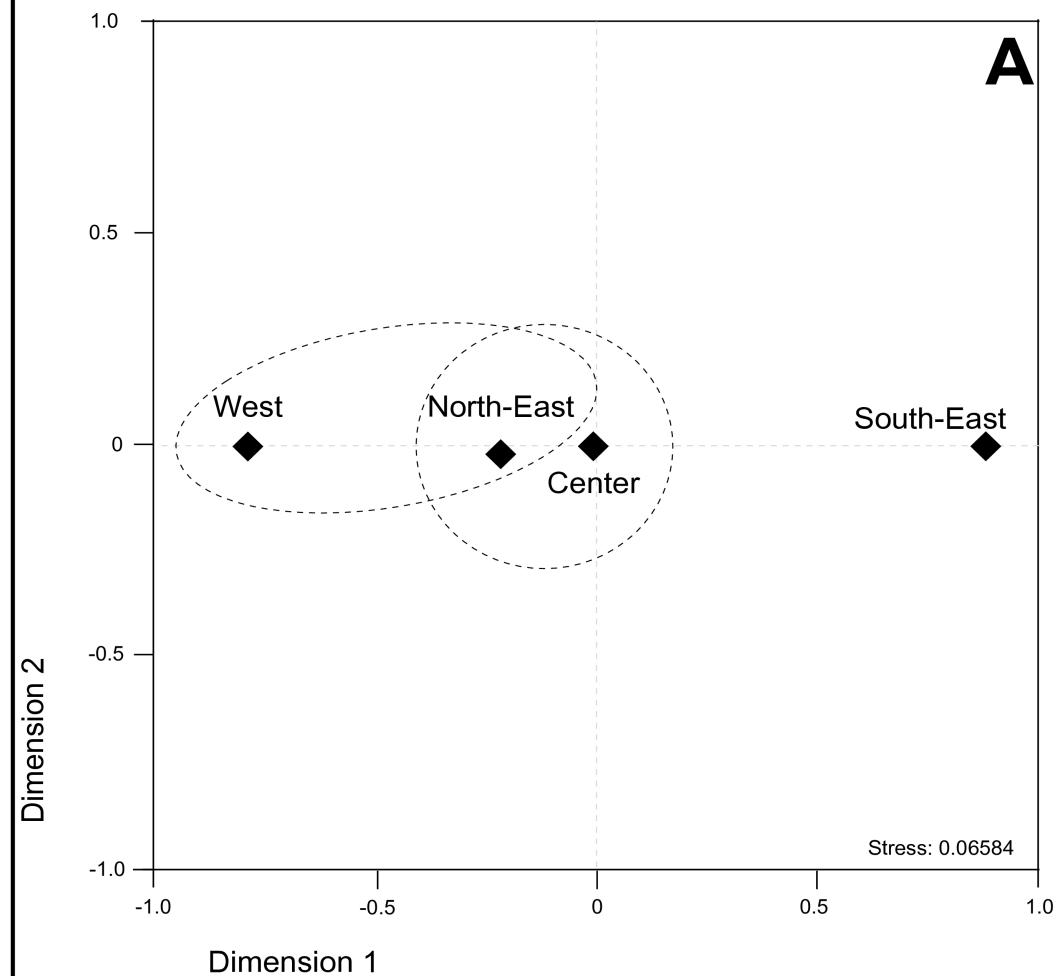
SUPPLEMENTAL INFORMATION TEXT

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Figure S1

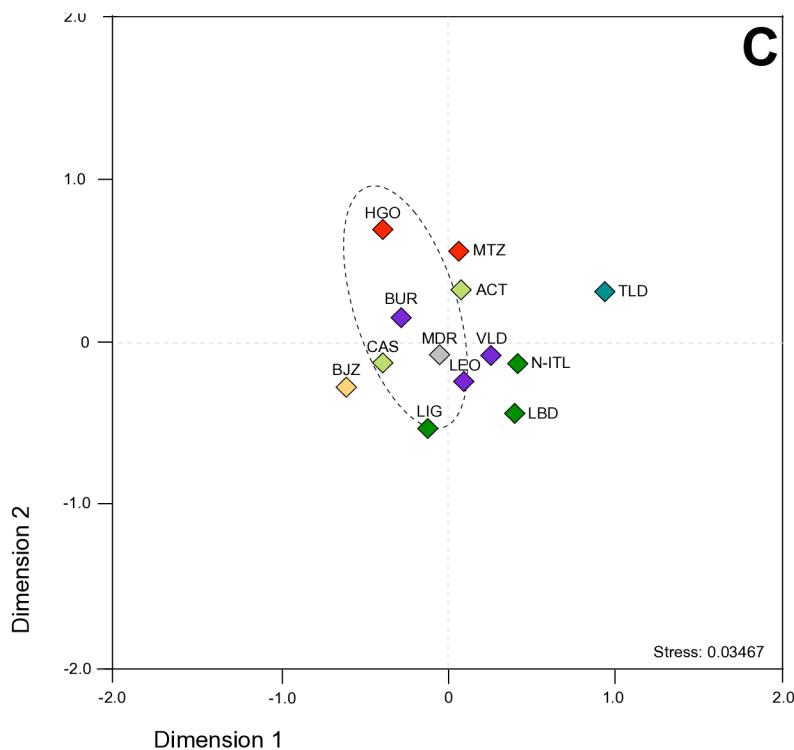
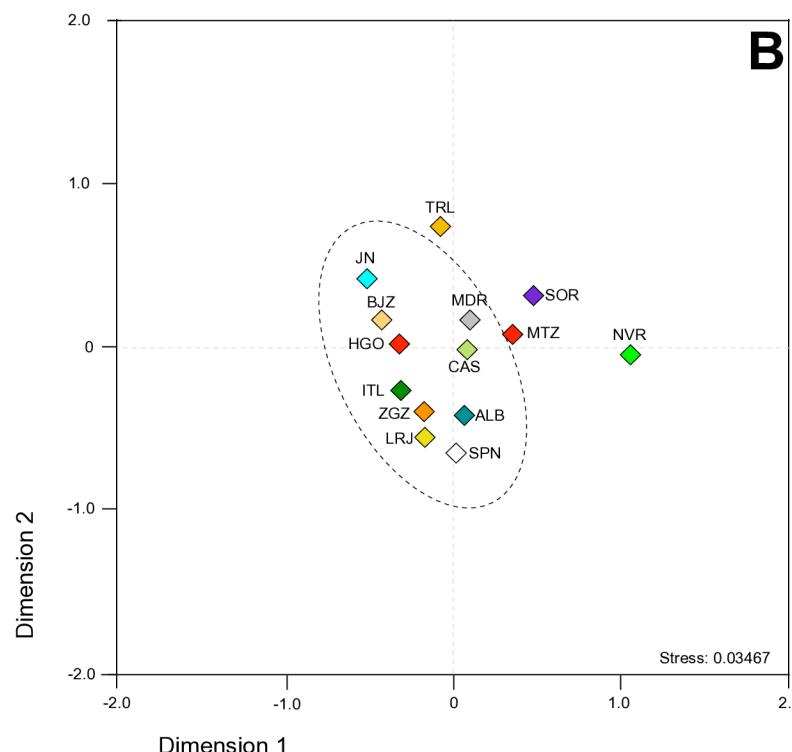
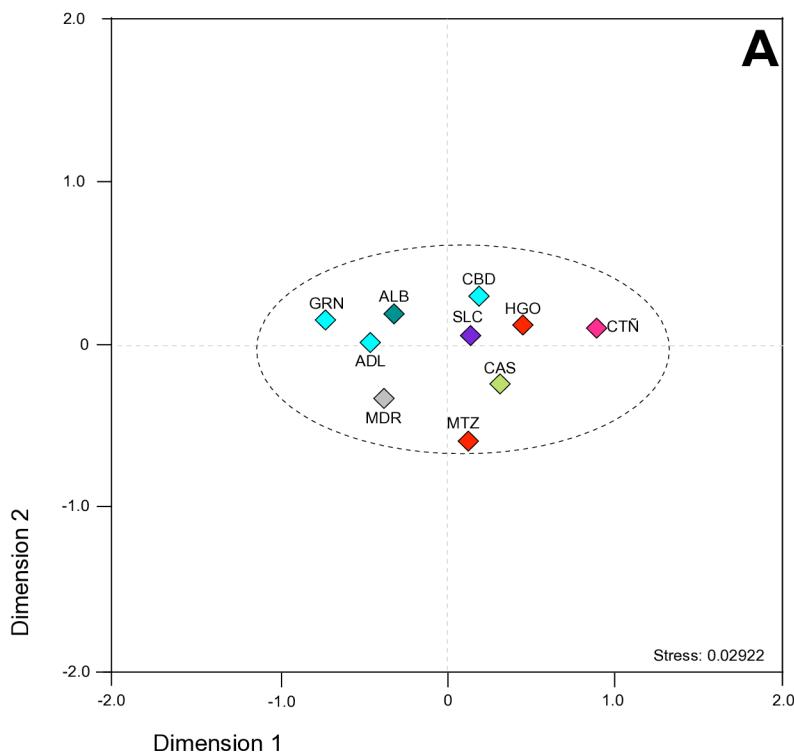


SUPPLEMENTAL FIGURE 1 LEGEND

Title: A MDS plot of R_{ST} values estimated using 17 Y-STRs haplotypes from haplogroup Q in Native Mexicans populations from the Central Valley of Mexico; related to Figures 1 and 2 and Table S3.

Note: (A) With the geography-1 criteria, Center (Hidalgo: *Hñähñús*, Nahuas, Tepehuas; Morelos: Nahuas; Puebla: Popolocas, Totonacas); West (Guanajuato: *Hñähñús*, *Éza'r*; Querétaro: *Hñähñús*); South-East (Veracruz, Totonacas); North-East (San Luis Potosí, Nahuas).

(B) With the geography-2 criteria, North-Central (Guanajuato: *Hñähñús*, *Éza'r*; Querétaro: *Hñähñús*; San Luis Potosí: Nahuas); Eastern (Hidalgo: *Hñähñús*, Nahuas, Tepehuas; Puebla: Popolocas, Totonacas; Veracruz: Totonacas); South-Central (Morelos: Nahuas). The dotted circle encloses populations that share no significant genetic distances.

Figure S2

Native and Mestizo Mexican populations

◆ Hidalgo (HGO); Mestizo (MTZ).

Spanish regions for comparisons

- ◆ Andalucía: Andalucía (ADL), Córdoba (CDB), Granada (GRN), Jaén (JN)
- ◆ Aragón: Zaragoza (ZGZ)
- ◆ Castilla La Mancha: Albacete (ALB), Toledo (TLD)
- ◆ Castilla y León: Burgos (BUR), León (LEO), Salamanca (SLC), Soria (SOR), Valladolid (VLD)
- ◆ Cataluña (CTN)
- ◆ Extremadura: Badajoz (BJZ)
- ◆ La Rioja: La Rioja (LRJ)
- ◆ Madrid (MDR)
- ◆ Navarra (NVR)
- ◆ Spain (SPN)
- ◆ Teruel (TRL)
- ◆ Valenciana: Alicante (ACT), Castellón (CAS)

Other Europeans

- ◆ Italy: Liguria (LIG), Lombardy (LBD), North Italy (N-ITL)

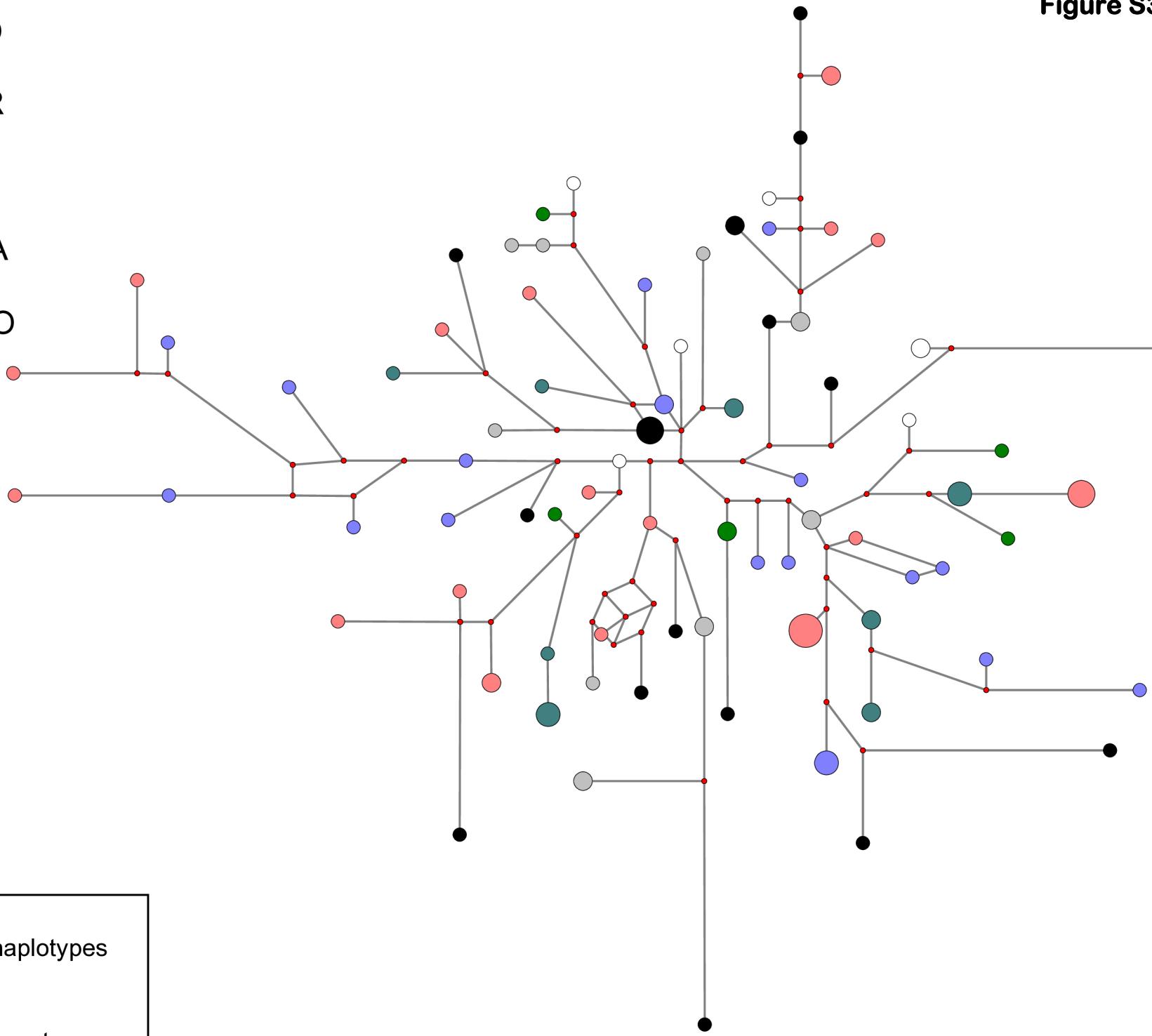
SUPPLEMENTAL FIGURE 2 LEGEND

Title: MDS plots of R_{ST} values estimated using 14 Y-STRs haplotypes from non-Native haplogroups in Native Mexican populations from the Central Valley of Mexico; related to Figure 3 and Table S7.

Note: (A) Haplogroup E; (B) Haplogroup I; and (C) Haplogroup J. The comparative data were taken from Martinez-Cadena et al., (2016), Martinez-Gonzalez et al., (2012), and Santana et al., (2014). The dotted circle encloses populations that share no significant genetic distances.

Figure S3

- Nahua HGO
- Nahua MOR
- Nahua SLP
- Nahua SnPA
- Nahua SnDO
- Nahua X
- Nahua Z



Number of haplotypes



One mutation step

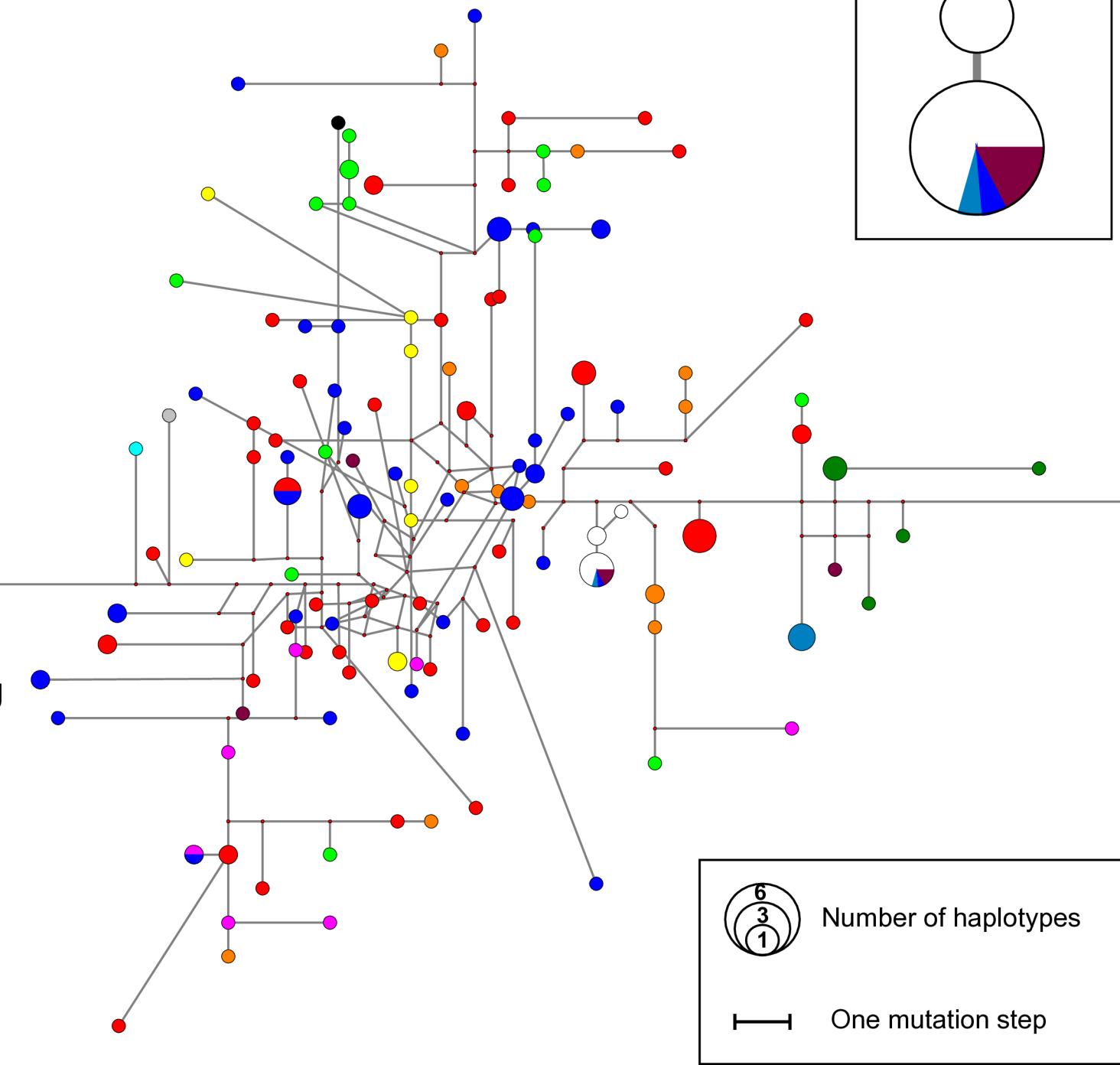
SUPPLEMENTAL FIGURE 3 LEGEND

Title: A median-joining network of Q1b1a1a (Q-M3) in Nahua populations using 17 Y-STR haplotypes. The phylogenetic analysis involved data from Nahua populations (separated by geographic region) from the present study and published data from Nahua populations living in other localities of Mexico; related to Figures 1 and 5 and Tables S3 and S9.

Note: The comparative data were obtained from Sandoval et al., (2012). HGO: Hidalgo state; SLP: San Luis Potosi state; MOR: Morelos state; SnPA: San Pedro Actopan (boundary between Mexico City and Morelos state); SnDO: Santo Domingo Ocotitlan (Morelos state); X: Xochimilco (southern Mexico City); Z: Zitlala (Guerrero state).

Figure S4

- Hñähñú
- Nahua
- Popoloca
- Tepehua
- Totonaca
- Úza'
- Canadian-Metis
- Gwich'in
- Haida
- Inuvialuit
- Seaconke-Wampanoag
- Tlicho
- Tlingit
- Wiyot

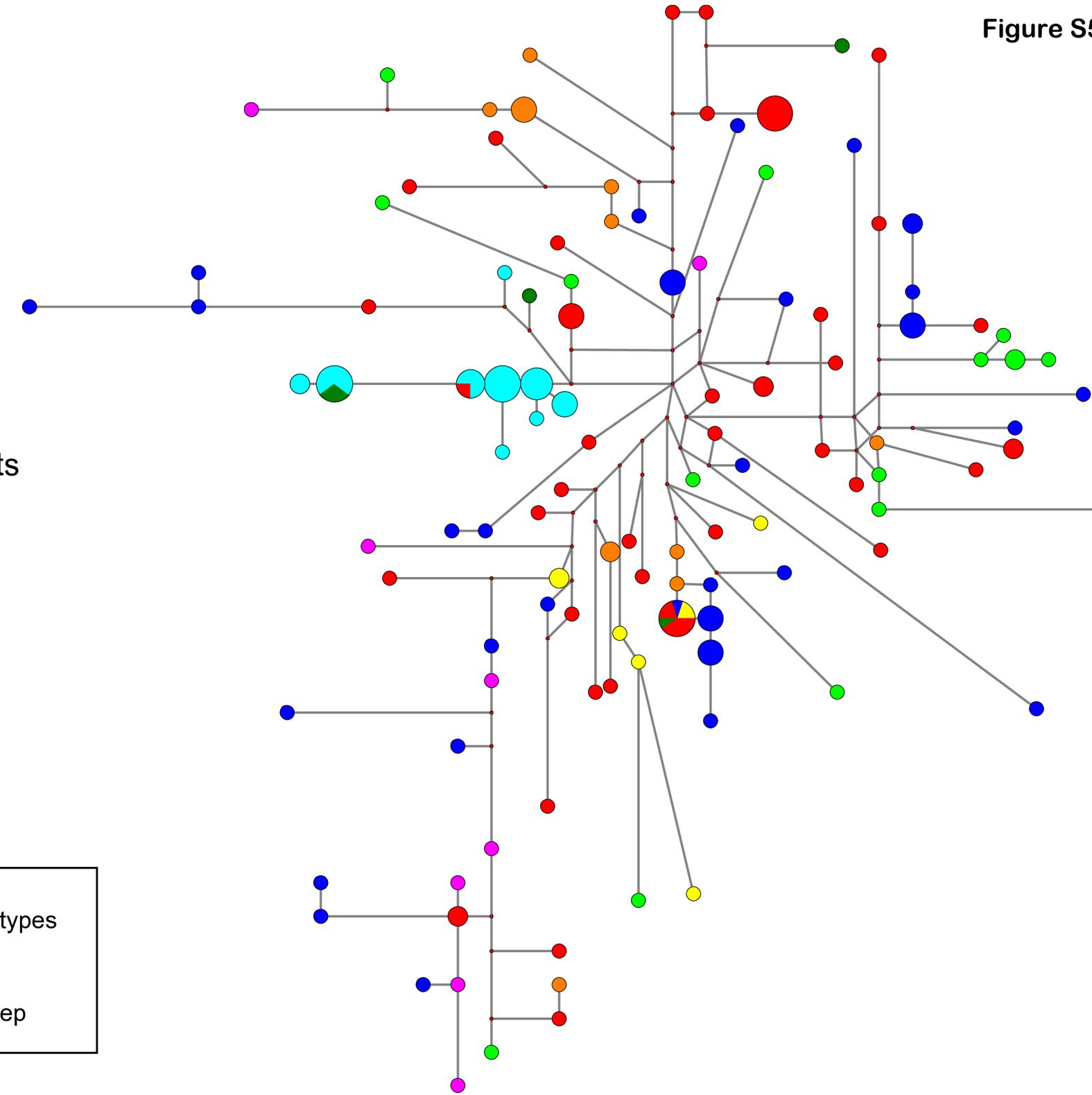
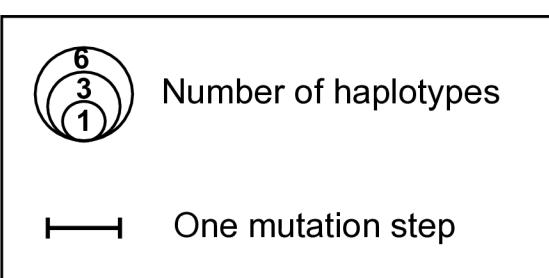
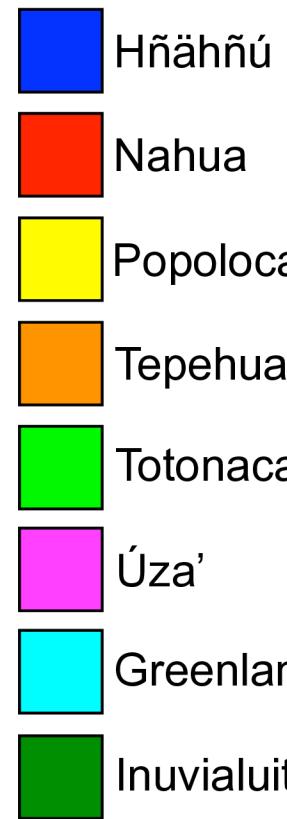


SUPPLEMENTAL FIGURE 4 LEGEND

Title: A median-joining network of Q1b1a1a (Q-M3) using 14 Y-STR haplotypes from Native Mexican and indigenous North American populations; related to Figures 1 and 5 and Table S9.

Note: The box shows the shared haplotypes at the center of the network. The comparative data were obtained from Dulik et al., (2012), Regueiro et al., (2013), and Schurr et al., (2012).

Figure S5

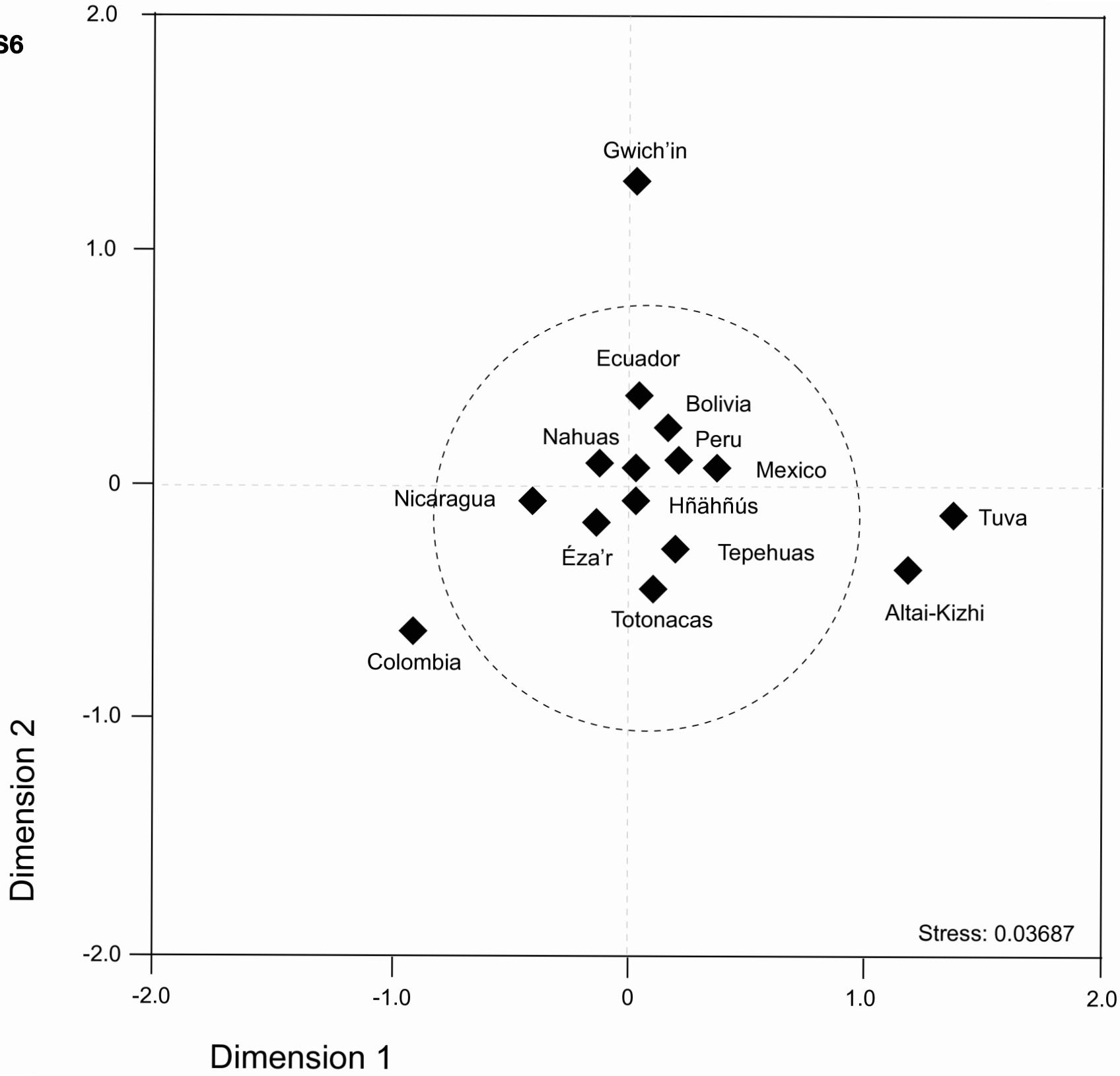


SUPPLEMENTAL FIGURE 5 LEGEND

Title: A median-joining network of Q1b1a1a (Q-M3) based on 17 Y-STR haplotypes in Native Mexicans, Greenland Inuits and Canadian Inuvialuit. Greenland Inuits encompass the East and West Semersooq, Kujalleq, Qeqqata, and Qaasuitsup populations; related to Figures 1 and 5 and Table S9.

Note: The comparative data were obtained from Dulik et al., (2012) and Oloffson et al., (2015).

Figure S6

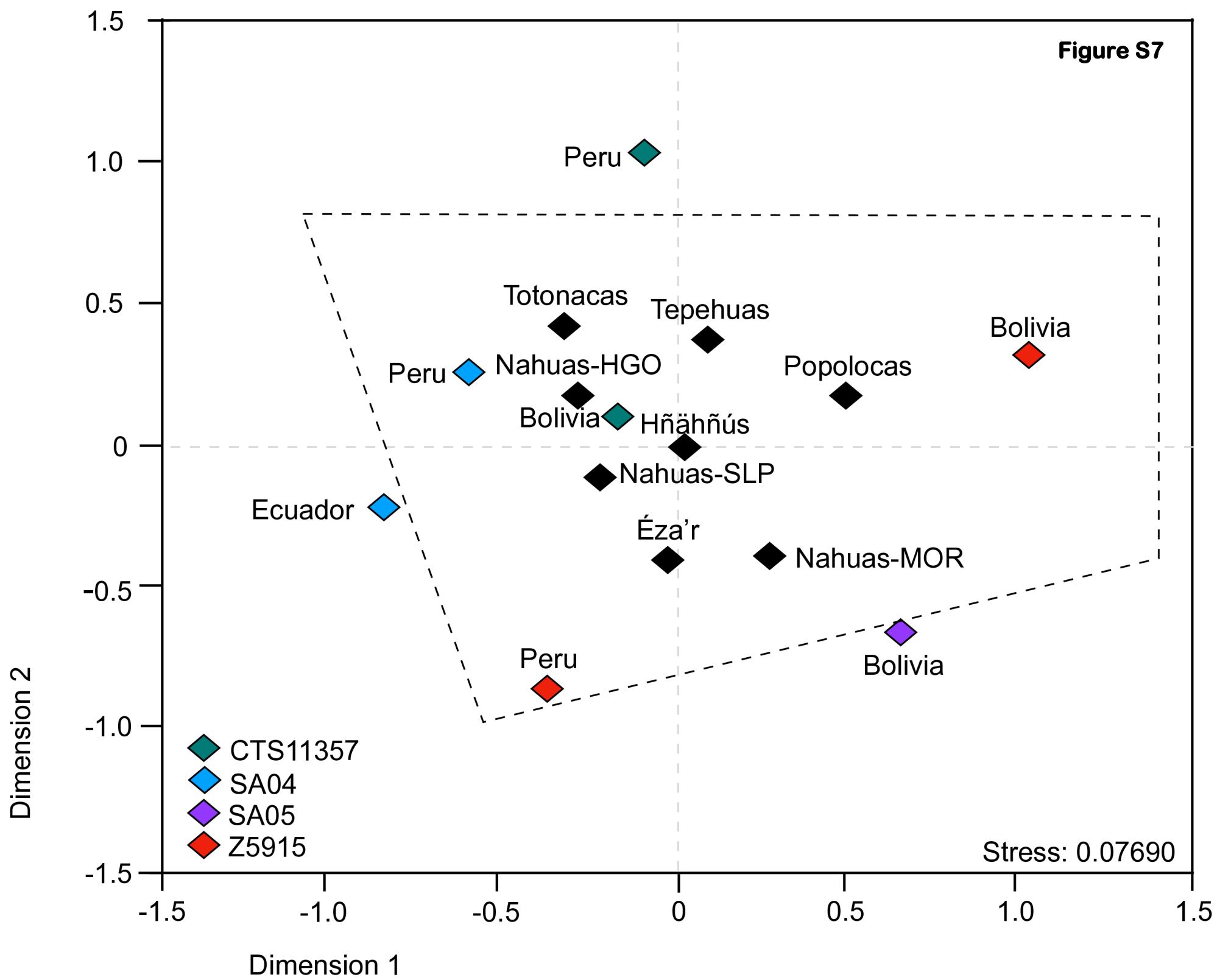


SUPPLEMENTAL FIGURE 6 LEGEND

Title: A MDS plot of R_{ST} values estimated from 14 Y-STRs haplotypes in Native Mexican and other Mesoamerican populations belonging to haplogroup Q1b1a1a (Q-M3); related to Figure 5 and Tables S9 and S10.

Note: The comparative data were obtained from Battaglia et al., (2013) and Nunez et al., (2012). The dotted circle encloses populations that share no significant genetic distances.

Figure S7



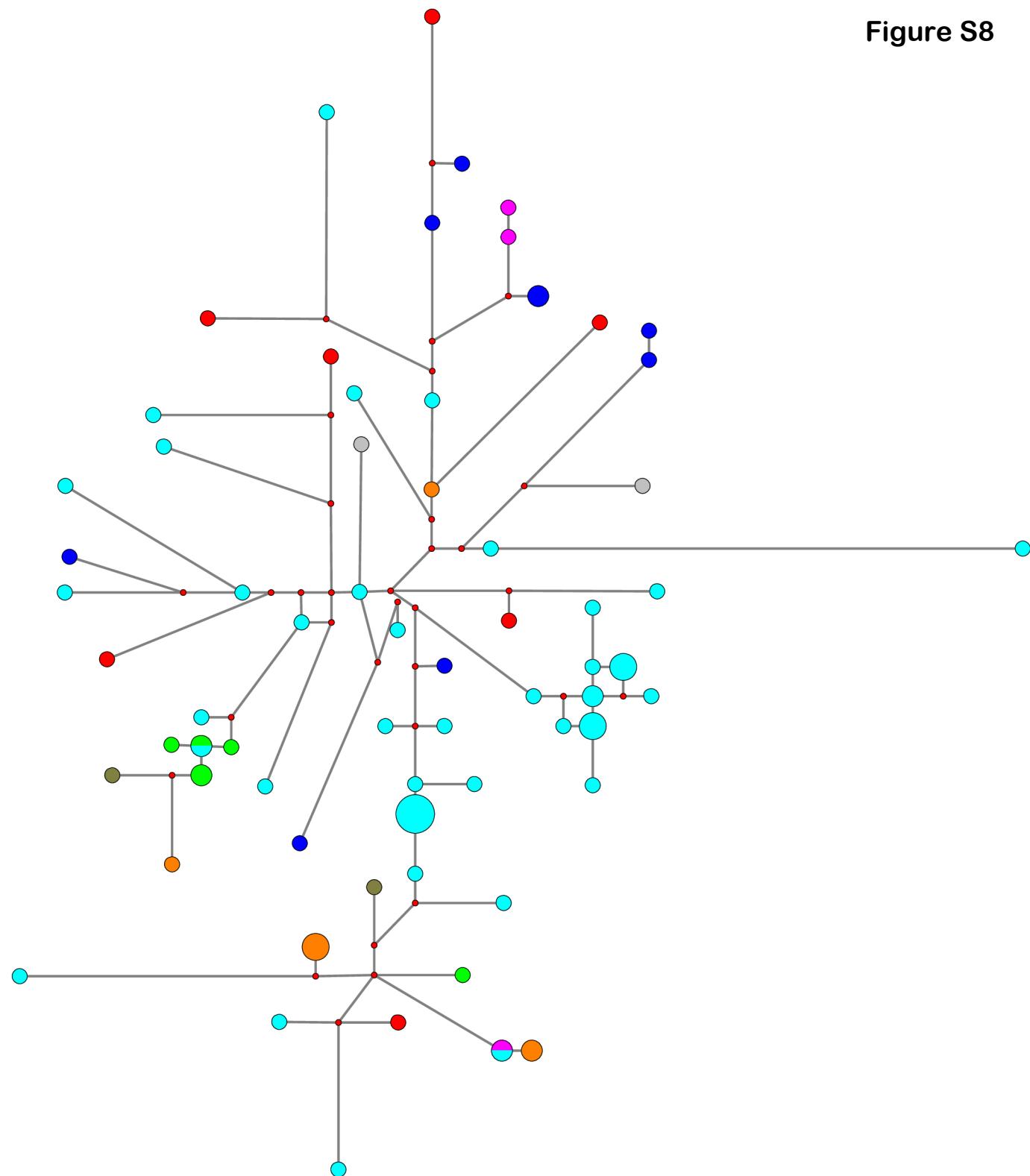
SUPPLEMENTAL FIGURE 7 LEGEND

Title: A MDS plot of R_{ST} values estimated from 14 Y-STRs haplotypes in Native Mexican and indigenous South American populations belonging to haplogroup Q1b1a1a (Q-M3); related to Figure 5 and Tables S9 and S11.

Note: The comparative data were obtained from Jota et al., (2016). The dotted circle encloses populations that share no significant genetic distances.

Figure S8

- █ Hñähñú
- █ Mexico
- █ Nahua
- █ Nicaragua
- █ Panama
- █ Tepehua
- █ Totonaca
- █ Úza'

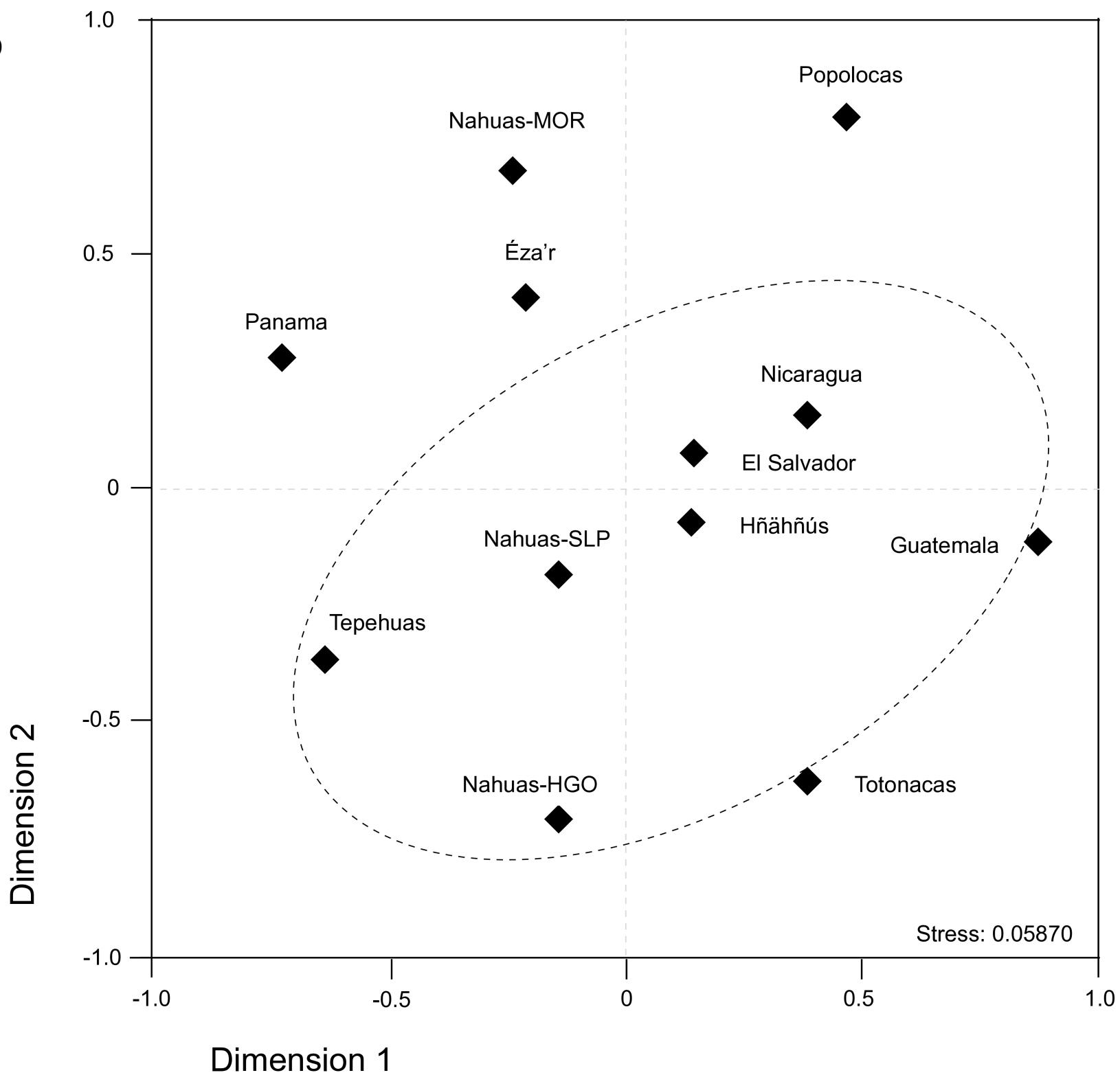


SUPPLEMENTAL FIGURE 8 LEGEND

Title: A median-joining network of Q1b1a2 (Q-Z777) based on 14 Y-STR haplotypes in Native Mexican and indigenous Mesoamerican populations; related to Figure 1 and Table S9.

Note: The comparative data were obtained from Battaglia et al., (2013).

Figure S9

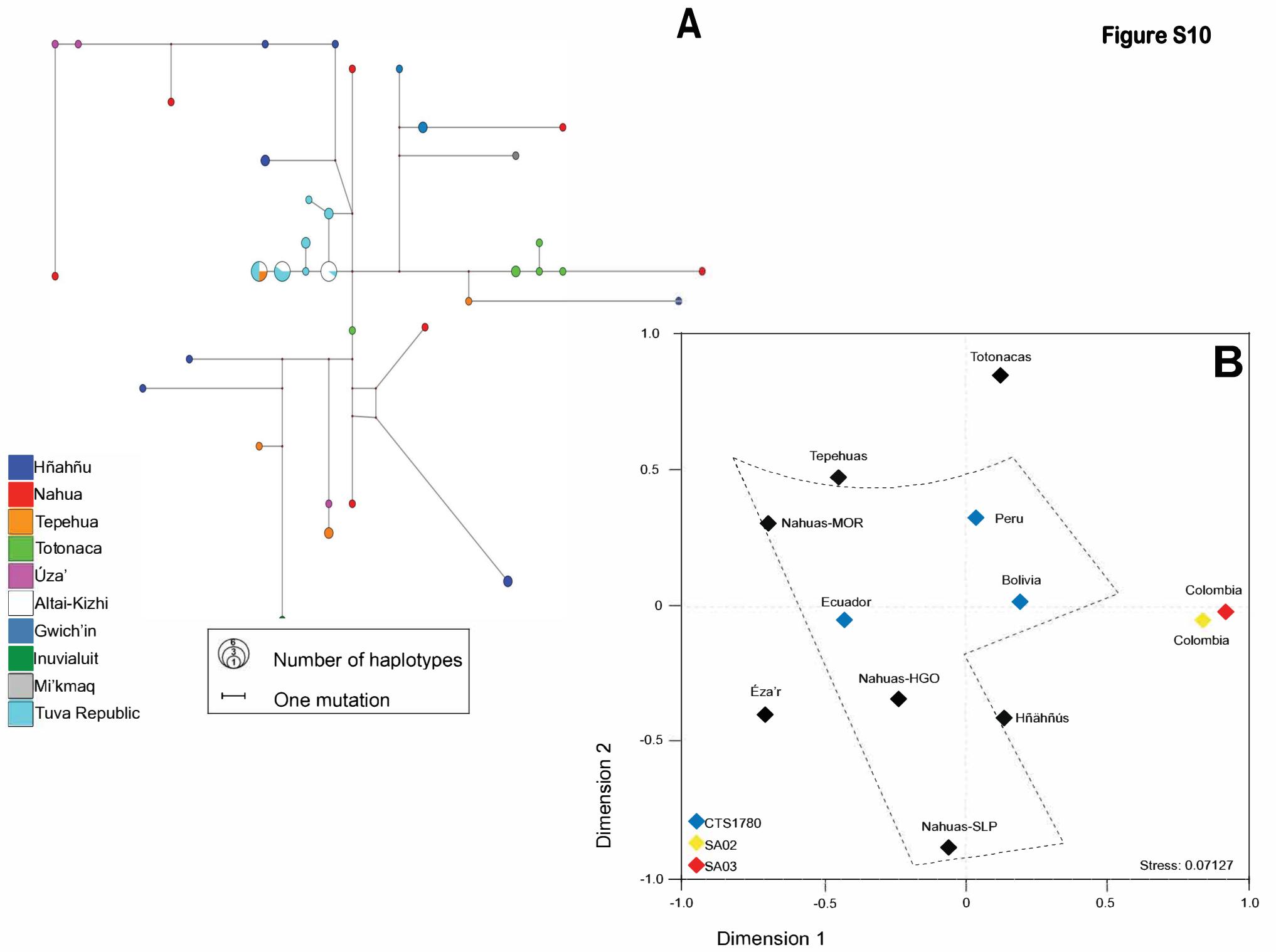


SUPPLEMENTAL FIGURE 9 LEGEND

Title: A MDS plot of R_{ST} values estimated from 14 Y-STRs haplotypes belonging to haplogroup Q-Z777/Z780 in Native Mexicans, indigenous populations from North, Central and South America, and Altai-Kizhi and Tuvan populations from Siberia; related to Figure 1 and Tables S9 and S12.

Note: The comparative data were obtained from Battaglia et al., (2013), Dulik et al., (2012a), Dulik et al., (2012b), and Regueiro et al., (2013). The dotted circle encloses populations that share no significant genetic distances.

Figure S10



SUPPLEMENTAL FIGURE 10 LEGEND

Title: Analysis of genetic diversity in haplogroup Q1b1a2 (Q-Z777/Z780); related to Figure 1 and Tables S9 and S13.

Note: (A). A median-joining network based on 15 Y-STR haplotypes in Native Mexican, indigenous North American and Asian populations; (B). A MDS plot of R_{ST} values estimated from 15 Y-STRs haplotypes from Q1b1a2 in Native Mexican and indigenous South American populations. The comparative data were obtained from Dulik et al., (2012a), Dulik et al., (2012b), Jota et al., (2016), and Regueiro et al., (2013). The dotted polygon encloses populations that show no significant genetic distances between them.

Table S1. Localities and ethnic groups sampled during the two expeditions.

Region	State	Localities	Geographic location	Ethnic groups	Linguistic family
NC	GTO	Rancho Uza, San Luis de la Paz	N 21° 17' 27.7" / W 100° 29' 34.5"	Chichimeca (Uza')	Oto-Manguean
CVM	HGO	Los Reyes, Acaxochitlan	N 20° 9' 19.8" / W 98° 9' 41"		
		La Mesa Limantilta, Huejutla	N 21° 4' 29.5" / W 98° 25' 16"		
		Tepetitla, Yahualica	N 20° 57' 38.1" / W 98° 23' 5.2"	Nahua	Uto-Aztecán
NC	SLP	Xoloco, Axtla de Terrazas	N 21° 28' 19.9" / W 98° 53' 45.2"		
SC	MOR	Cuentepec, Temixco	N 18° 52' 00" / W 99° 19' 38.3"		
		Yonte Chico, Alfajayucan	N 20° 24' 30.2" / W 99° 19' 40.5"		
		La Florida, Cardonal	N 20° 30' 46.9" / W 99° 00' 0.4"		
	HGO	El Alberto, Ixmiquilpan	N 20° 24' 41.9" / W 99° 12' 47.1"		
		La Lagunita, Ixmiquilpan	N 20° 39' 57.2" / W 99° 14' 27.2"		
		San Juan Tlatepexi, Mezquital	N 20° 34' 2.4" / W 98° 53' 53.1"		
CVM		Huisticola, Metztitlán	N 20° 38' 0.4" / W 98° 49' 00"		
		Bocua, Nicolás Flores	N 20° 43' 31.3" / W 99° 10' 0.7"	Otomí (Hñähñú)	
		San Miguel, San Bartolo Tutotepec	N 20° 26' 29.7" / W 98° 12' 6.9"		
		Portezuelo, Tasquillo	N 20° 29' 14.7" / W 99° 18' 25.2"		
		Pañhé, Tecozautla	N 20° 31' 2.9" / W 99° 41' 12.6"		
		Xajha, Zimapán	N 20° 45' 52.7" / W 99° 29' 38.3"		
NC	GTO	Cieneguilla, Tierra Blanca	N 21° 4' 51" / W 100° 10' 56.7"		
	QRO	Cuicillo, Amealco de Bonfil	N 20° 8' 15.8" / W 99° 56' 37"		
		Santa Inés Ahuatepec	N 18° 24' 53.5" / W 98° 1' 23.2"		
SC	PUE	San Felipe Otlaltepec, Tepexi de Rodríguez	N 18° 24' 20.5" / W 97° 54' 44.2"	Popoloca	
CVM	HGO	Huehuetla, Tenango de Doria	N 20° 27' 41.4" / W 98° 3' 59.1"	Tepehua	
SC	PUE	Huehuetla, Francisco I. Madero	N 18° 24' 20.5" / W 97° 54' 44.2"		
E	VER	Plan de Hidalgo, Papantla	N 20° 23' 58.8" / W 97° 26' 24.2"	Totonaca	Totozoquean
		Zozocolco de Hidalgo	N 20° 8' 1" / W 97° 35' 56.7"		

SUPPLEMENTAL TABLE 1 LEGEND

Title: Localities and ethnic groups sampled during fieldwork expeditions; related to Figure 1.

Note: CVM, Central Valley of Mexico; E, Eastern; NC, North-Central; SC, South-Central; GTO, Guanajuato; HGO, Hidalgo; MOR, Morelos; PUE, Puebla; QRO, Querétaro; SLP, San Luis Potosí; VER, Veracruz; N, North; W, West.

Table S2. Frequency of Y-STR haplotypes from Amerindian and non-Amerindian lineages found in the study populations.

SUPPLEMENTAL TABLE 2 LEGEND

Title: Frequency of Y-chromosome haplogroups in the study populations; related to Figure 1.

Note: GTO, Guanajuato; HGO, Hidalgo; MOR, Morelos; PUE, Puebla; QRO, Querétaro; SLP, San Luis Potosí; VER, Veracruz. “Hg” = haplogroup; “n” = sample size.

Table S4. AMOVA based on geographiy using 17 Y-STR haplotypes from haplogroup Q in Native American populations

	Percentage of variation	p-value
Hñähñús		
Among populations	0.92	0.378
Within populations	99.08	< 0.0001
Nahuas		
Among populations	4.29	0.009
Within populations	95.71	< 0.0001
Totonacas		
Among populations	0.21	0.377
Within populations	99.79	< 0.0001

SUPPLEMENTAL TABLE 4 LEGEND

Title: AMOVA estimates based on geography using haplogroup Q Y-STR haplotypes in Native Mexican populations; related to Table 2.

Note: Y-STR haplotypes were based on 17 STR loci. The *p* values shown in bold indicate significant values.

Table S5. RST values estimated from haplogroup Q 17 Y-STR haplotypes in Native Mexican populations categorized by ling

	Oto-Manguean	Uto-Aztecán	Totonaca-Tepehuan
Oto-Manguean	-	0.19582	0.02213
Uto-Aztecán	0.00525	-	0.02213
Totonaca-Tepehuan	0.02418	0.02553	-

SUPPLEMENTAL TABLE 5 LEGEND

Title: R_{ST} values estimated from haplogroup Q Y-STR haplotypes in Native Mexican populations categorized by linguistic affiliation; related to Figure 2.

Note: Y-STR haplotypes were defined by 17 STR loci. GTO, Guanajuato; HGO, Hidalgo; MOR, Morelos; PUE, Puebla; QRO, Querétaro; SLP, San Luis Potosí; VER, Veracruz. Oto-Manguean: *Éza'r, Hñahñús* (from HGO, GTO, and QRO), and Popolocas; Totonaca-Tepehua: Tepehuas and Totonacas from PUE and VER; Uto-Aztecans: Nahuas from HGO, MOR and SLP. The R_{ST} values are presented in the lower diagonal of the table, while the p values appear in the upper matrix. These estimates were generated with Arlequin v3.5 (10,000 permutations) and adjusted by false discovery rate test in R-software. The p values in boldface indicate significantly different values.

Table S6. RST values estimated from haplogroup Q Y-STR haplotypes in Native Mexican populations based on ethnicity.

	Éza'r	Hñähñús	Nahuas-HGO	Nahuas-MOR	Nahuas-SLP	Popolocas	Tepehuas	Totonacas
Éza'r	-	0.0273	0.0126	0.5889	0.1666	0.0273	0.0755	0.0218
Hñähñús	0.0926	-	0.3887	0.1249	0.4791	0.0055	0.2875	0.2440
Nahuas-HGO	0.1284	0.0091	-	0.0273	0.2440	≤ 0.0001	0.2440	0.0436
Nahuas-MOR	-0.0143	0.0736	0.1276	-	0.3250	0.2156	0.2440	0.1249
Nahuas-SLP	0.0481	0.0010	0.0164	0.0235	-	0.0553	0.1574	0.0947
Popolocas	0.1818	0.1497	0.2473	0.0965	0.1346	-	0.0218	0.0273
Tepehuas	0.0898	0.0113	0.0192	0.0469	0.0428	0.1724	-	0.2078
Totonacas	0.1742	0.0271	0.0448	0.1296	0.0603	0.2071	0.0413	-

SUPPLEMENTAL TABLE 6 LEGEND

Title: R_{ST} values estimated from haplogroup Q Y-STR haplotypes in Native Mexican populations based on ethnicity; related to Figure 2.

Note: Y-STR haplotypes were defined by 17 STR loci. HGO, Hidalgo; MOR, Morelos; SLP, San Luis Potosí. R_{ST} values are presented in the lower diagonal of the table, whereas *p* values appear in the upper diagonal. These estimates were obtained with Arlequin v3.5 (10,000 steps in Markov chain and 1000 demorization steps) and adjusted by false discovery rate test in R-software. The *p* values shown in boldface indicate significant differences.

Table S7. Non-Amerindian Y-STR haplotypes for the Central Valley of Mexico ethnicities and lineage data.

#	Hg	FREQUENCY						Y-STR Haplotype																		SNPs		
		HÑÄHÑÚ	NAHUA	POPOLOCA	TEPEHUA	TOTONACA	ÚZÁ'	D D Y S Y S 2 3 8 9 5 a b	D D Y S Y S 2 3 8 9 5 I	D D Y S Y S 3 3 3 9 0	D D Y S Y S 3 3 3 9 1	D D Y S Y S 3 3 3 9 2	D D Y S Y S 3 3 3 9 3	D D Y S Y S 3 3 3 9 7	D D Y S Y S 3 3 3 9 8	D D Y S Y S 3 3 3 9 9	D D Y S Y S 3 3 3 9 8	D D Y S Y S 3 3 3 9 6	D D Y S Y S 3 3 3 9 8	D D Y S Y S 3 3 3 9 5	D D Y S Y S 3 3 3 9 4	Y G A T A H 4	D Y S 4	D Y S 3	M17G	M343A		
3		1						13 13 17 17 18 18 19 19	15 17 18 18 19 19 20 20	18 18 18 19 19 19 20 20	13 12 13 13 14 14 13 14	17 24 24 24 24 24 24 24	10 10 11 11 11 11 11 11	10 11 13 13 14 14 13 14	11 11 13 13 14 14 13 14	13 14 14 14 14 14 13 14	14 14 14 14 14 14 13 14	10 10 10 10 10 10 11 10	12 10 10 10 10 10 11 11	20 20 20 20 20 20 20 20	20 20 20 20 20 20 16 17	17 14 14 14 14 14 20 20	16 14 14 14 14 14 17 20	23 22 22 22 22 22 13 13	12 11 11 11 11 11 11 12	- -	- -	
5	E-M96	1						13 13 17 17 18 18 19 19	15 17 18 18 19 19 20 20	18 18 18 19 19 19 20 20	13 12 13 13 14 14 13 14	17 24 24 24 24 24 24 24	10 10 11 11 11 11 11 11	11 11 13 13 14 14 13 14	13 14 14 14 14 14 13 14	14 14 14 14 14 14 13 14	10 10 10 10 10 10 11 10	10 10 10 10 10 10 11 10	20 20 20 20 20 20 20 20	17 14 14 14 14 14 16 17	16 14 14 14 14 14 17 20	23 22 22 22 22 22 13 13	11 11 11 11 11 11 11 12	- -	- -			
6		1						13 13 17 17 18 18 19 19	15 17 18 18 19 19 20 20	18 18 18 19 19 19 20 20	13 12 13 13 14 14 13 14	17 24 24 24 24 24 24 24	10 10 11 11 11 11 11 11	11 11 13 13 14 14 13 14	13 14 14 14 14 14 13 14	14 14 14 14 14 14 13 14	10 10 10 10 10 10 11 10	10 10 10 10 10 10 11 10	20 20 20 20 20 20 20 20	14 14 14 14 14 14 16 15	14 14 14 14 14 14 17 22	22 22 22 22 22 22 11 11	11 11 11 11 11 11 11 12	- -	- -			
52		1						15 15 18 18 19 19 20 20	18 18 19 19 20 20 21 21	19 19 20 20 21 21 22 22	14 14 15 15 16 16 17 17	18 24 24 24 24 24 24 24	10 10 11 11 11 11 11 11	11 11 13 13 14 14 13 14	13 14 14 14 14 14 13 14	14 14 14 14 14 14 13 14	10 10 10 10 10 10 11 10	11 11 11 11 11 11 12 11	20 20 20 20 20 20 20 20	16 14 14 14 14 14 17 20	20 14 14 14 14 14 17 20	13 11 11 11 11 11 11 12	- -	- -				
4	E1b1b						1	13 13 16 16 17 17 17 17	16 17 17 17 18 18 19 19	17 17 18 18 19 19 20 20	13 13 14 14 15 15 16 16	17 24 24 24 24 24 24 24	10 10 11 11 11 11 11 11	11 11 13 13 14 14 13 14	13 14 14 14 14 14 13 14	14 14 14 14 14 14 13 14	10 10 10 10 10 10 11 10	13 13 13 13 13 13 12 11	20 20 20 20 20 20 21 21	15 15 15 15 15 15 14 14	14 14 14 14 14 14 17 22	22 22 22 22 22 22 12 12	11 11 11 11 11 11 11 12	- -	- -			
36	G-M201	1						14 15 15 15	14 13 13 13	14 16 16 16	14 12 12 12	17 21 21 21	22 21 20 20	10 10 11 11	11 11 15 15	13 15 16 16	16 16 16 16	11 10 10 10	11 13 13 13	19 24 24 24	14 15 15 16	17 15 16 16	22 21 21 21	12 11 11 12	- -	- -		
45		1						15 15 13 13	13 13 16 16	16 16 18 18	12 12 12 12	17 21 21 21	21 21 20 20	10 10 11 11	11 11 15 15	15 15 16 16	16 16 16 16	10 10 10 10	13 13 13 13	24 24 24 24	15 15 16 16	17 16 16 16	21 21 21 21	11 11 12 12	- -	- -		
46		2						15 15 13 13	13 13 16 16	16 16 18 18	12 12 12 12	17 21 21 21	21 21 20 20	10 10 11 11	11 11 15 15	15 15 16 16	16 16 16 16	10 10 10 10	13 13 13 13	24 24 24 24	16 16 16 16	16 16 21 21	21 21 11 11	11 11 12 12	- -	- -		
41	G2a	1						15 15 10 10	10 10 17 17	17 17 12 12	12 12 17 17	22 22 22 22	22 22 20 20	10 10 11 11	11 11 13 13	13 13 16 16	16 16 10 10	10 10 11 11	11 11 21 21	21 21 16 16	17 17 16 16	21 21 21 21	12 12 11 11	12 12 11 11	- -	- -		
50	I-M170	1						15 15 16 16	16 16 18 18	18 18 14 14	14 14 18 18	22 22 22 22	22 22 20 20	10 10 12 12	12 12 14 14	14 14 15 15	15 15 10 10	10 10 11 11	20 20 20 20	13 13 18 18	18 18 21 21	21 21 11 11	13 13 11 11	- -	- -			
57	I2a1	1						17 17 12 12	12 12 14 14	12 12 15 15	14 14 25 25	25 25 9 9	9 9 11 11	13 13 13 13	13 13 15 15	15 15 10 10	10 10 12 12	12 12 21 21	21 21 14 14	14 14 15 15	22 22 15 15	22 22 11 11	13 13 11 11	- -	- -			
49	I2b1						1	15 15	16 16	17 17	13 13	16 16	23 23	10 10	12 12	15 15	14 14	10 10	11 11	20 20	14 14	18 18	23 23	11 11	12 12	- -	- -	
51		1						15 15	16 16	18 18	14 14	18 18	22 22	10 10	12 12	14 14	15 15	10 10	11 11	20 20	13 13	18 18	21 21	11 11	12 12	- -	- -	
28	J-M304	1						14 14 14 14 14	11 13 14 14 14	15 18 18 18 18	13 13 13 13 13	17 23 23 23 23	23 23 23 23 23	10 10 11 11 11	11 11 13 13 13	12 12 13 13 13	14 14 14 14 14	10 10 10 10 10	12 12 12 12 12	21 21 21 21 21	15 14 15 15 15	17 14 15 15 15	21 21 21 21 21	11 11 12 12 12	- -	- -		
34		1						14 14 14 14 14	13 13 14 14 14	18 18 18 18 18	13 13 13 13 13	16 16 16 16 16	23 23 23 23 23	10 10 11 11 11	11 11 13 13 13	13 13 14 14 14	14 14 14 14 14	10 10 10 10 10	12 12 12 12 12	20 20 20 20 20	14 14 15 15 15	19 14 15 15 15	22 22 21 21 21	11 11 11 12 12	- -	- -		
37		1						14 14 14 14 14	14 14 14 14 14	16 16 16 16 16	13 13 13 13 13	23 23 23 23 23	23 23 23 23 23	10 10 11 11 11	11 11 12 12 12	12 12 13 13 13	15 15 15 15 15	9 9 9 9 9	12 12 12 12 12	21 21 21 21 21	15 15 15 15 15	17 15 15 15 15	21 21 21 21 21	12 12 11 11 15	- -	- -		
38		1						14 14 14 14 14	14 14 14 14 14	18 18 18 18 18	13 13 13 13 13	16 16 16 16 16	23 23 23 23 23	10 10 11 11 11	11 11 12 12 12	12 12 13 13 13	14 14 14 14 14	10 10 10 10 10	11 11 11 11 11	20 20 20 20 20	15 15 15 15 15	18 18 18 18 18	20 20 20 20 20	11 11 11 11 16	- -	- -		
40		1						14 14 14 14 14	16 16 16 16 16	18 18 18 18 18	12 12 12 12 12	16 16 16 16 16	24 24 24 24 24	10 10 11 11 11	11 11 12 12 12	12 12 13 13 13	14 14 14 14 14	9 9 9 9 9	12 12 12 12 12	19 19 19 19 19	14 14 14 14 14	17 17 17 17 17	20 20 20 20 20	11 11 11 11 15	- -	- -		
27	J1	2						14 14 14 14 14	11 13 13 13 13	15 18 18 18 18	13 13 13 13 13	16 16 16 16 16	23 23 23 23 23	10 10 11 11 11	11 11 12 12 12	12 12 13 13 13	14 14 14 14 14	10 10 10 10 10	12 12 12 12 12	21 21 21 21 21	15 16 17 17 17	17 21 21 21 21	11 11 11 11 16	- -	- -			
35	J2a1b				1			14 14 14 14 14	13 13 13 13 13	18 18 18 18 18	13 13 13 13 13	16 16 16 16 16	23 23 23 23 23	10 10 11 11 11	11 11 12 12 12	12 12 13 13 13	16 16 16 16 16	9 9 9 9 9	11 11 11 11 11	20 20 20 20 20	15 15 15 15 15	17 17 17 17 17	23 23 23 23 23	11 11 11 11 15	- -	- -		
39	L				1			14 14 14 14 14	16 16 16 16 16	17 17 17 17 17	14 14 14 14 14	16 16 16 16 16	23 23 23 23 23	10 10 11 11 11	14 14 12 12 12	12 12 13 13 13	15 15 10 10 10	10 10 11 11 10	20 20 20 20 20	14 14 14 14 14	16 16 16 16 16	21 21 21 21 21	10 10 11 11 12</td					

SUPPLEMENTAL TABLE 7 LEGEND

Title: Non-native Y-STR haplotypes for Native Mexican populations from the Central Valley of Mexico; related to Figure 3.

Note: These samples were also screened for the M17 and M343 SNPs that define R1a1 and R1b, respectively. The haplogroups to which these haplotypes belong and the ethnic groups in which they appear are indicated therein.

Table S10. Rst values estimated from Q-M3 Y-STR haplotypes in Native Mexican and Mesoamerican populations.

	Éza'r	Nahuas-HGO	Nahuas-MOR	Nahuas-SLP	Hñähñús	Panama	Popolocas	Tepehuas
Éza'r	-	≤ 0.0001	0.9315	0.3193	0.1239	≤ 0.0001	0.0396	0.0991
Nahuas-HGO	0.1582	-	≤ 0.0001	0.1416	0.2803	≤ 0.0001	≤ 0.0001	≤ 0.0001
Nahuas-MOR	-0.0655	0.2018	-	0.2939	0.2201	0.0811	0.2027	0.0811
Nahuas-SLP	0.0203	0.0236	0.0294	-	0.9575	≤ 0.0001	0.0240	0.0577
Hñähñús	0.0541	0.0054	0.0405	-0.0147	-	≤ 0.0001	0.0631	0.1419
Panama	0.1353	0.1897	0.1419	0.1073	0.1056	-	≤ 0.0001	≤ 0.0001
Popolocas	0.2057	0.2749	0.1166	0.1503	0.1150	0.2188	-	≤ 0.0001
Tepehuas	0.1365	0.0976	0.1682	0.0696	0.0420	0.1340	0.2255	-
Totonacas	0.1707	0.0387	0.1802	0.0832	0.0647	0.2875	0.2724	0.1592
El Salvador	-0.1672	0.0656	-0.0244	-0.1151	-0.2920	-0.1212	-0.0117	0.0823
Nicaragua	0.0941	0.0409	0.1105	0.0429	0.0194	0.0989	0.1080	0.0839
Guatemala	0.1955	0.2796	0.3378	0.0795	0.0736	0.2778	0.1876	0.2789

Totonacas **El Salvador** **Nicaragua** **Guatemala**

0.0396	0.9910	0.0496	0.0396
0.1416	0.9910	0.0721	0.2803
0.1297	0.9910	0.1216	0.0811
0.0240	0.9910	0.0577	0.8649
≤ 0.0001	0.9910	0.1766	0.3048
≤ 0.0001	0.9910	≤ 0.0001	0.1081
≤ 0.0001	0.9910	≤ 0.0001	0.0676
0.0451	0.9910	≤ 0.0001	0.0601
-	0.9910	≤ 0.0001	0.4460
-0.1264	-	0.6396	0.6396
0.1183	-0.2123	-	0.6396
0.1136	-0.1539	0.0871	-

SUPPLEMENTAL TABLE 10 LEGEND

Title: R_{ST} values estimated from Q-M3 Y-STR haplotypes in Native Mexican and Mesoamerican populations; related to Figure 5 and Figure S6.

Note: Y-STR haplotypes were defined by 14 STR loci. HGO, Hidalgo; MOR, Morelos; SLP, San Luis Potosí. R_{ST} values are presented in the lower diagonal, while p values appear in the upper diagonal. All estimates were obtained with Arlequin v3.5 (10,000 steps in Markov chain and 1000 demorization steps) and adjusted by false discovery rate test in R-software. The p values shown in boldface indicate significant differences.

Table S11. Rst values estimated Q-M3 Y-STR haplotypes in Native Mexican and indigenous and

	Hñähñús	Nahuas-HGO	Nahuas-SLP	Popolocas	Totonacas
Hñähñús	-	0.2626	0.9910	0.0609	0.0168
Nahuas-HGO	0.0094	-	0.3764	≤ 0.0001	0.0852
Nahuas-SLP	-0.0231	0.0106	-	0.0316	0.0852
Popolocas	0.1102	0.2708	0.1358	-	≤ 0.0001
Totonacas	0.0784	0.0546	0.0789	0.2724	-
Tepehuas	0.0485	0.0642	0.0520	0.2140	0.1013
Éza'r	0.0438	0.1574	0.0371	0.2408	0.1940
Nahuas-MOR	0.0665	0.2276	0.0472	0.1184	0.2262
Bolivia-Z5915	0.1371	0.4088	0.2598	0.2474	0.4048
Peru-Z5915	-0.0086	0.2365	0.0301	0.3218	0.2191
Peru-SA04	-0.2307	0.0576	-0.2105	0.1308	-0.0134
Ecuador-SA04	0.1418	0.2985	0.1799	0.4082	0.2443
Bolivia-SA05	0.1828	0.2672	0.2505	0.4036	0.3813
Peru-CTS11357	0.1195	0.2502	0.1910	0.3629	0.2141
Bolivia-CTS11357	-0.2038	-0.1315	-0.1907	0.1609	-0.0838

admixed South American populations.

Tepehuas	Éza'r	Nahuas-MOR	Bolivia-Z5915	Peru-Z5915	Peru-SA04
0.0748	0.2539	0.1330	0.9910	0.9910	0.9910
0.0168	≤ 0.0001	≤ 0.0001	0.9910	0.9910	0.9910
0.1099	0.2062	0.1833	0.9910	0.9910	0.9910
≤ 0.0001	0.0168	0.1099	0.9910	0.9910	0.9910
0.0852	≤ 0.0001	0.0316	0.9910	0.9910	0.9910
-	0.1216	0.0466	0.9910	0.9910	0.9910
0.0923	-	0.8218	0.9910	0.9910	0.9910
0.1278	-0.0352	-	0.9910	0.9910	0.9910
0.3622	0.4452	0.5882	-	0.9910	0.9910
0.2940	0.2833	0.5254	1.0000	-	0.9910
-0.0018	0.2037	0.3636	1.0000	1.0000	-
0.2552	0.2842	0.4013	0.6417	0.4275	0.2020
0.3987	0.4507	0.5115	0.5170	0.4647	0.5627
0.2754	0.4982	0.6158	0.8449	0.7829	0.7286
0.0017	0.0575	0.2373	0.3333	0.2414	-0.1579

Ecuador-SA04	Bolivia-SA05	Peru-CTS11357	Bolivia-CTS11357
≤ 0.0001	≤ 0.0001	0.0316	0.9910
≤ 0.0001	≤ 0.0001	≤ 0.0001	0.9910
≤ 0.0001	≤ 0.0001	0.0168	0.9910
≤ 0.0001	≤ 0.0001	≤ 0.0001	0.2834
≤ 0.0001	≤ 0.0001	≤ 0.0001	0.8142
≤ 0.0001	≤ 0.0001	≤ 0.0001	0.4309
0.0195	≤ 0.0001	≤ 0.0001	0.4438
≤ 0.0001	≤ 0.0001	0.0195	0.1578
0.1578	0.1791	0.1791	0.4438
0.2683	0.1495	0.1856	0.9907
0.4725	0.1405	0.1495	0.9910
-	≤ 0.0001	≤ 0.0001	0.1856
0.5534	-	≤ 0.0001	0.0195
0.5409	0.5703	-	0.2683
0.3815	0.4044	0.4358	-

SUPPLEMENTAL TABLE 11 LEGEND

Title: R_{ST} values estimated Q-M3 Y-STR haplotypes in Native Mexican and indigenous South American populations; related to Figure 5 and Figure S7.

Note: Y-STR haplotypes were defined by 14 STR loci. HGO, Hidalgo; MOR, Morelos; SLP, San Luis Potosí. R_{ST} values are presented in the lower diagonal, and p values appear in the upper diagonal. All estimates were obtained with Arlequin v3.5 (10,000 steps in Markov chain and 1000 demorization steps) and adjusted by false discovery rate test in R-software. The p values shown in boldface indicate significant differences. Populations with CTS11357, SA04, SA05, and Z5915 SNPs in their Q-M3 haplotypes are indicated in the table header.

Table S12. RST values estimated from Q-L54 Y-STR haplotypes in Native Mexicans, indigenous American and Asian populations

	Altai-Kizhi	Bolivia	Éza'r	Colombia	Ecuador	Gwich'in	Mexico	Nahuas	Nicaragua
Altai-Kizhi	-	≤ 0.0001	0.0097						
Bolivia	0.4355	-	0.0878	≤ 0.0001	0.2538	≤ 0.0001	≤ 0.0001	0.1562	0.5045
Éza'r	0.5961	0.2249	-	0.0691	0.0797	0.1684	0.1957	0.8469	0.4351
Colombia	0.7941	0.5205	0.6348	-	≤ 0.0001	≤ 0.0001	≤ 0.0001	≤ 0.0001	0.0565
Ecuador	0.6210	0.0188	0.2768	0.6162	-	≤ 0.0001	0.0243	0.3181	0.3514
Gwich'in	0.8485	0.4159	0.7149	0.7728	0.5812	-	≤ 0.0001	0.0374	0.0716
Mexico	0.3758	0.1453	0.1307	0.4975	0.0986	0.4001	-	0.3114	0.2115
Nahuas	0.4393	0.0437	-0.1256	0.5247	0.0115	0.3438	0.0137	-	0.6073
Nicaragua	0.6430	0.0310	0.1539	0.5926	0.0984	0.6667	0.0986	-0.0187	-
Hñähñús	0.4459	0.0752	-0.1081	0.4835	0.0866	0.3967	0.1016	-0.0272	-0.0299
Panama	0.7301	0.1446	0.0192	0.1281	0.3442	0.5909	0.1780	0.0480	0.0417
Peru	0.4036	0.0071	0.1534	0.5296	0.0217	0.4330	0.1321	0.0221	0.0825
Tepehuas	0.4840	0.1431	0.1361	0.6094	0.2218	0.7029	0.1070	0.0809	0.0506
Totonacas	0.6419	0.1172	0.2937	0.6411	0.1377	0.8419	0.1110	0.0934	0.1498
Tuva Repub.	0.1221	0.4805	0.6894	0.8279	0.6963	0.8815	0.4129	0.5292	0.7393

ons.

Hñähñús	Panama	Peru	Tepehuas	Totonacas	Tuva
≤ 0.0001	0.0180	≤ 0.0001	≤ 0.0001	≤ 0.0001	0.0097
0.0390	0.2236	0.2236	0.0390	0.0502	≤ 0.0001
0.6781	0.6781	0.1105	0.3054	0.1036	0.0207
≤ 0.0001	0.1957	≤ 0.0001	≤ 0.0001	≤ 0.0001	≤ 0.0001
0.1158	0.0374	0.2230	0.0608	0.1024	≤ 0.0001
≤ 0.0001	0.1095	≤ 0.0001	0.0487	0.0374	≤ 0.0001
0.0243	0.1216	≤ 0.0001	0.0811	0.0487	≤ 0.0001
0.6073	0.3027	0.3211	0.3211	0.3211	≤ 0.0001
0.4742	0.7297	0.3211	0.4742	0.1261	≤ 0.0001
-	0.4606	0.1261	0.3211	0.3211	≤ 0.0001
0.0205	-	0.2911	0.3211	0.1261	≤ 0.0001
0.0436	0.1592	-	0.1261	0.1261	≤ 0.0001
0.0300	0.1904	0.1067	-	0.3027	≤ 0.0001
0.0351	0.4161	0.0783	0.1366	-	≤ 0.0001
0.4958	0.7687	0.4403	0.5226	0.7278	-

SUPPLEMENTAL TABLE 12 LEGEND

Title: R_{ST} values estimated from Q-L54 Y-STR haplotypes in Native Mexicans, indigenous American and Asian populations; related to Figure 6 and Figure S9.

Note: Y-STR haplotypes were defined by 14 STR loci. R_{ST} values appear in the lower diagonal, whereas p values appear in the upper diagonal. All estimates were obtained with Arlequin v3.5 (10,000 steps in Markov chain and 1000 demorization steps) and adjusted by false discovery rate test in R-software. The p values shown in boldface indicate significant differences.

Table S13. RST values estimated Q-L54 Y-STR haplotypes in Native Mexican and indigenous South American populations.

	Nahuas-HGO	Nahuas-SLP	Tepehuas	Totonacas	Hñähñús	Nahuas-MOR	Éza'r	Colombia-SA02
Nahuas-HGO	-	0.99099	0.13215	0.09911	0.79279	0.99099	0.94144	≤ 0.0001
Nahuas-SLP	0.10687	-	0.31531	0.31531	0.31531	0.99099	0.31531	0.31531
Tepehuas	0.1605	0.44856	-	0.01622	0.04054	0.99099	0.09266	≤ 0.0001
Totonacas	0.37201	0.6	0.38677	-	≤ 0.0001	0.99099	0.04805	≤ 0.0001
Hñähñús	-0.00569	0.14195	0.14437	0.34757	-	0.99099	0.12613	≤ 0.0001
Nahuas-MOR	-0.17	1	-0.33333	0.58095	-0.18421	-	0.25676	0.25676
Éza'r	-0.03885	0.40299	0.17198	0.51678	0.12949	0.28571	-	0.02253
Colombia-SA02	0.6828	0.90426	0.74056	0.86278	0.59442	0.91469	0.84582	-
Colombia-SA03	0.33143	1	0.55333	0.79535	0.30651	1	0.61905	-1.25
Bolivia-CTS1780	0.02012	0.33128	0.23363	0.39472	0.09797	0.12348	0.28045	0.59066
Ecuador-CTS1780	0.04847	0.35948	0.23642	0.44603	0.12467	0.19008	0.3317	0.74386
Peru-CTS1780	-0.01793	0.33786	0.16945	0.33781	0.08173	0.00728	0.21821	0.60251

Colombia- SA03	Bolivia- CTS1780	Ecuador- CTS1780	Peru- CTS1780
0.99099	0.59459	0.4955	0.79279
0.99099	0.31531	0.31531	0.31531
0.99099	≤ 0.0001	≤ 0.0001	≤ 0.0001
0.99099	≤ 0.0001	0.01442	≤ 0.0001
0.99099	0.02102	0.09459	≤ 0.0001
0.99099	0.25676	0.25676	0.4
0.99099	0.02253	0.02253	0.02253
0.99099	≤ 0.0001	≤ 0.0001	≤ 0.0001
-	0.05406	0.0991	0.05406
0.46906	-	0.26126	0.26126
0.61265	0.0207	-	0.24324
0.48557	0.00631	0.01422	-

SUPPLEMENTAL TABLE 13 LEGEND

Title: R_{ST} values estimated Q-L54 Y-STR haplotypes in Native Mexican and indigenous South American populations; related to Figure 6 and Figure S10.

Note: Y-STR haplotypes were defined by 15 STR loci. HGO, Hidalgo; MOR, Morelos; SLP, San Luis Potosí. R_{ST} values appear in the lower diagonal, whereas p values appear in the upper diagonal. All estimates were obtained with Arlequin v3.5 (10,000 steps in Markov chain and 1000 demorization steps) and adjusted by false discovery rate test in R-software. The p values shown in boldface indicate significant differences. Populations with CTS1780, SA02, and SA03 SNPs in their Q-L54 haplotypes are indicated in the table header.